

Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro  
 450 455 460

5 Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly  
 465 470 475 480

Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu  
 485 490 495

10 Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn  
 500 505 510

Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser  
 515 520 525

15 Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val  
 530 535 540

20 Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile  
 545 550 555 560

Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn  
 565 570 575

25 Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln  
 580 585 590

Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp  
 595 600 605

30 Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp  
 610 615 620

35 Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn  
 625 630 635 640

Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val  
 645 650 655

40 Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys  
 660 665 670

Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu  
 675 680 685

45 Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro  
 690 695 700

50 Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp  
 705 710 715 720

Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu  
 725 730 735

	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	
				740					745					750			
5	Ala	Tyr	Thr	Arg	Tyr	Glu	Leu	Arg	Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	
			755					760					765				
	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	Asn	Ala	Lys	His	Glu	Ile	Val	Asn	
		770					775					780					
10	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	Pro	Leu	Ser	Ala	Gln	Ser	Pro	Ile	
	785					790					795					800	
	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg	Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	
				805						810					815		
15	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	Asp	Gly	Glu	Lys	Cys	Ala	His	His	
			820						825						830		
	Ser	His	His	Phe	Thr	Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	
20			835					840						845			
	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile	Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	
		850					855						860				
25	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	Phe	Leu	Glu	Glu	Lys	Pro	Leu	Leu	
	865					870					875					880	
	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys	Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	
				885						890					895		
30	Lys	Arg	Glu	Lys	Leu	Gln	Leu	Glu	Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	
			900						905					910			
	Lys	Glu	Ser	Val	Asp	Ala	Leu	Phe	Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	
35			915					920					925				
	Gln	Val	Asp	Thr	Asn	Ile	Ala	Met	Ile	His	Ala	Ala	Asp	Lys	Arg	Val	
		930					935					940					
40	His	Arg	Ile	Arg	Glu	Ala	Tyr	Leu	Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	
	945					950					955					960	
	Val	Asn	Ala	Ala	Ile	Phe	Glu	Glu	Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	
				965						970					975		
45	Tyr	Ser	Leu	Tyr	Asp	Ala	Arg	Asn	Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	
			980						985					990			
	Asn	Gly	Leu	Leu	Cys	Trp	Asn	Val	Lys	Gly	His	Val	Asp	Val	Glu	Glu	
50			995				1000						1005				
	Gln	Asn	Asn	His	Arg	Ser	Val	Leu	Val	Ile	Pro	Glu	Trp	Glu	Ala	Glu	
		1010					1015					1020					

Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg  
1025 1030 1035 1040

5 Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His  
1045 1050 1055

Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu  
1060 1065 1070

10 Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly  
1075 1080 1085

15 Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr  
1090 1095 1100

Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser  
1105 1110 1115 1120

20 Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys  
1125 1130 1135

Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr  
1140 1145 1150

25 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile  
1155 1160 1165

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu  
1170 1175 1180

30 Leu Leu Met Glu Glu  
1185

35 (2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3567

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

50 ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT  
Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser  
1 5 10 15

48